Amendment

Please enter the following amendments to the claims. This listing of claims replaces all prior listings of claims in the application.

1-7. (Canceled)

8. (Previously presented) The method according to claim 13 or claim 14 wherein the restriction site is specific for a class IIs enzyme.

9. (Previously presented) The method according to claim 8, wherein the enzyme is SfaNI or EarI.

10. (Previously presented) The method according to claim 13 or claim 14, wherein the polymerase reaction is carried out using methyl-dCTP as a replacement for dCTP.

11. (Previously presented) The method according to claim 13 or claim 14, wherein the adapter is immobilised on a support material.

12. (Previously presented) The method according to claim 13 or 14, wherein sequential signal sequences and optionally sequential adapters comprise recognition sites for different oligonucleotide primers.

13. (Currently amended) A method for determining the sequence of a target polynucleotide, comprising the steps of:

i) treating a sample of a double-stranded target polynucleotide to create overhangs at each end, a first end which is the end to be sequenced and a second end which is not to be sequenced~~one of which is to be sequenced~~, each overhang having a defined number of bases;

ii) dividing the sample into reaction compartments and contacting each separate sample with a double-stranded polynucleotide signal sequence and a corresponding double stranded adapter polynucleotide, each signal sequence representing a specific polynucleotide sequence of the same length as that of the overhang at the first end that is to be sequenced and comprising an overhang that permits hybridisation and ligation to the second end of the

target polynucleotide ~~opposite that being sequenced~~, and each adapter comprising an overhang that is of complementary sequence to the sequence represented by the signal sequence, wherein the adapter will hybridise to the overhang at the first end of~~on~~ the target sample that is to be sequenced only if the sequence of the adapter overhang is complementary thereto ~~to the overhang that is being sequenced~~;

iii) carrying out the polymerase reaction on the sample (s) using primers that hybridise at the ends of the signal sequence and adapter sequence, wherein the product of the polymerase reaction comprises a restriction site that permits cleavage of the adapter to form a new overhang to be sequenced optionally by repeating steps (i) to (iii) using restriction enzymes to create the overhangs;

and iv) identifying which signal sequences are present on the amplified products, and in which order, to thereby determine the sequence of the target polynucleotide.

14. (Previously presented) The method according to claim 13, wherein the overhang that ligates to the signal sequence is at least 3 bases.

15. (Previously presented) The method according to claim 13 or claim 14, wherein the overhang to be sequenced is 4 bases.

16. (Previously presented) The method according to claim 13 or claim 14, wherein the combination of all the sequences represented by the signal sequence in each reaction compartment corresponds to all the permutations of a sequence comprising the number of bases in the overhang to be sequenced.